### Sunday, January 15th, 2017

**Course:** Zero In on Tumor and Cancer NGS Data Analysis  
**Instructor:** Prof. Wang Lusheng  
**Place:** 204

| Time               | Session 1: Genomic Data Analysis  
|--------------------|----------------------------------  
| 10:00am - 12:00pm  | (Session Chair: Prof. Byung-Jun Yoon)  
|                    | Efficient Algorithms for Genomic Duplication Models  
|                    | (Jaroslaw Paszek and Pawel Gorecki)  
| 10:25am - 10:50am  | Genome Rearrangement with ILP  
|                    | (Tom Hartmann, Nicolas Wieseke, Roded Sharan, Martin Middendorf and Matthias Bernt)  
| 10:50am - 11:15am  | PECC: correcting contigs based on paired-end read distribution  
|                    | (Min Li, Xiaodong Yan, Junwei Luo, Fangxiang Wu, Yi Pan and Jianxin Wang)  
| 11:15am - 12:00pm  | Coffee Break (Lobby)  
| 12:00pm - 12:30pm  | Complimentary Lunch  
| 12:30pm - 14:30pm  | From Genotype to Phenotype: A Five-track Species-focused Biology Converges the Complexity of Life  
|                    | Keynote Speech: Prof. Jun Yu  
| 14:30pm - 15:30pm  | Coffee Break (Lobby)  
| 15:30pm - 15:55pm  | Bioinformatics for Cancer Immunotherapy  
|                    | Dr. Miao Li

**Virus Analysis in Cancer**  
Dr. Wenlong Jia

### Monday, January 16th, 2017

**Opening Remarks**

**Application of NGS and bioinformatics in response of infectious disease outbreaks**  
Keynote Speech: Dr. Tong Yi-Gang

| Time               | Session 1: Genomic Data Analysis  
|--------------------|----------------------------------  
| 10:25am - 10:50am  | Efficient Algorithms for Genomic Duplication Models  
|                    | (Jaroslaw Paszek and Pawel Gorecki)  
| 10:50am - 11:15am  | Visualization of consensus genome structure without using a reference genome  
|                    | (Ipputa Tada, Yasuhiro Tanizawa and Masanori Arita)  
| 11:15am - 12:00pm  | Coffee Break (Lobby)  
| 12:00pm - 12:30pm  | Complimentary Lunch  
| 12:30pm - 14:30pm  | From Genotype to Phenotype: A Five-track Species-focused Biology Converges the Complexity of Life  
|                    | Keynote Speech: Prof. Jun Yu  
| 14:30pm - 15:30pm  | Coffee Break (Lobby)  
| 15:30pm - 15:55pm  | Bioinformatics for Cancer Immunotherapy  
|                    | Dr. Miao Li
## Parallel Session

### Session 3: Evolution
**Session Chair: Prof. Tzong Yi Lee**

**15:55pm - 16:20pm**
- Gene Tree Construction and Correction using SuperTree and Reconciliation
  (Manuel Lafond, Cedric Chauve, Nadia El-Mabrouk and Aida Ouangraoua)

**16:20pm - 16:45pm**
- Live Phylogeny with Polytomies: Finding the Most Compact Parsimonious Trees
  (Dimitris Papamichail, Angela Huang, Edward Kennedy, Jan-Lucas Ott, Andrew Miller and Georgios Papamichail)

**16:45am - 17:10am**
- Coffee Break (Lobby)

**17:10pm - 17:35pm**
- Evolutionary model for the statistical divergence of paralogous and orthologous gene pairs generated by whole genome duplication and speciation
  (Yue Zhang, Chunfang Zheng and David Sankoff)

**17:35pm - 18:00pm**
- A Program to Compute the Soft Robinson–Foulds Distance between Phylogenetic Networks
  (Bingxin Lu, Louxin Zhang and Hon Wai Leong)

**18:00pm - 20:00pm**
- On-site Banquet with Dinner Speech
  (open and complimentary to all registered attendees)

### Session 4: NGS data Analysis
**Session Chair: Prof. Kyungsook Han**

**15:55pm - 16:20pm**
- Fuwa: a decision-tree-based fast variant caller for next-generation sequencing data
  (Zhentang Li, Yi Wang and Fei Wang)

**16:20pm - 16:45pm**
- Optimal hybrid sequencing and assembly: feasibility conditions for accurate genome reconstruction and cost minimization strategy
  (Chun-Chi Chen, Noushin Ghaffari, Xiaoning Qian and Byung-Jun Yoon)

**16:45am - 17:10am**
- Coffee Break (Lobby)

**17:10pm - 17:35pm**
- A framework for space-efficient read clustering in metagenomic samples
  (Jarno Alanko, Djamal Belazzougui, Fabio Cunial and Veli Mäkinen)

**17:35pm - 18:00pm**
- A Feature Sampling Strategy for Analysis of High Dimensional Genomic Data
  (Jie Zhang, Zhigen Zhao, Kai Zhang and Zhi Wei)

**Tuesday, January 17th, 2017**

### Parallel Session

### Session 5: Virus Analysis and Horizontal Gene Transfer
**Session Chair: Prof. Leong Hon Wai**

**09:00am - 09:25am**
- BATVI: Fast, Sensitive and Accurate Detection of Virus Integrations
  (Chandana Tennakoon and Wing-Kin Sung)

**09:25am - 09:50am**
- Inferring gene-species assignments in the presence of horizontal gene transfer
  (Agnieszka Mykowiecka, Pawel Gorecki)

**09:50am - 10:15am**
- Prediction of virus-host infectious association by supervised learning methods
  (Mengge Zhang, Lianping Yang, Jie Ren, Nathan Ahlgren, Jed Fuhrman and Fengzhu Sun)

**10:15am - 10:40am**
- Coffee Break (Lobby)

### Session 6: Parallel Tools and non-omics Data
**Session Chair: Prof. Limsoon Wong**

**09:00am - 09:25am**
- Parallel Identification of Variable-length Patterns for Large-scale Prediction of Protein-protein Interactions Using MapReduce
  (Lun Hu, Xiaohui Yuan, Pengwei Hu and Keith C. C. Chan)

**09:25am - 09:50am**
- P-Hint-Hunt: A Deep Parallelized Whole Genome DNA Methylation Detection Tool
  (Ming Gao, Xiangke Liao, Chengkun Wu, Wenguang Yu and Shaoliang Peng)

**09:50am - 10:15am**
- A novel wearable device for continuous, non-invasive blood pressure measurement
  (Qin Xin, Jianping Wu and Ke Xu)

### Parallel Session

### Session 7: Analysis Tools and Statistical Methodology Development
**Session Chair: Prof. Dongbo Bu**

### Session 8: Analysis Tools
**Session Chair: Prof. Yang Yang**
<table>
<thead>
<tr>
<th>Time</th>
<th>Session 9: 3D structures</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:40am - 11:05am</td>
<td>AfterQC: Automatic Filtering, Trimming, Error Removing and Quality Control for Fastq Data (Shifu Chen, Tanxiao Huang, Yanqing Zhou, Mingyan Xu and Jia Gu)</td>
</tr>
<tr>
<td>11:05am - 11:30am</td>
<td>Reviving the two-state Markov chain approach (Andrzej Mizera, Jun Pang and Qixia Yuan)</td>
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<tr>
<td>11:30am - 11:55am</td>
<td>DTL Reconciliation Repair (Weiyun Ma, Dmitriy Smirnov and Ran Libeskind-Hadas)</td>
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<tr>
<td>11:55am - 14:00pm</td>
<td>Complimentary Lunch</td>
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**Parallel Session**

**Session Chair: Dr. Tianhai Tian**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session 10: miRNA Analysis</th>
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</thead>
<tbody>
<tr>
<td>14:00pm - 14:25pm</td>
<td>Receptor-guided 3D-QSAR studies, Molecular Dynamics Simulation and Free energy calculations of Btk kinase inhibitors (Pavithra Balasubramanian, Anand Balupuri and Seung Joo Cho)</td>
</tr>
<tr>
<td>14:25pm - 14:50pm</td>
<td>SheddomeDB: the ectodomain shedding database for membrane-bound shed markers (Wei-Sheng Tien, Jun-Hong Chen and Kun-Pin Wu)</td>
</tr>
<tr>
<td>14:50pm - 15:15pm</td>
<td>Improving prediction of burial state of residues by exploiting correlation among residues (Hai’E Gong, Haicang Zhang, Chao Wang, Shiwei Sun, Wei-Mou Zheng, Dongbo Bu and Jianwei Zhu)</td>
</tr>
<tr>
<td>15:15pm - 15:30pm</td>
<td>Coffee Break (Lobby)</td>
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**Parallel Session**

**Session Chair: Dr. Lun Hu**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session 11: Analysis</th>
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<tbody>
<tr>
<td>15:30pm - 15:55pm</td>
<td>An integrated approach with new strategies for QSAR models and lead optimization (Hui-Hui Hsu, Li-Jen Chang and Jim-Moon Yang)</td>
</tr>
<tr>
<td>15:55pm - 16:20pm</td>
<td>Negative Sampling with Multi-Layer Perceptron for Biological Event Trigger Identification (Nan Jiang, Wenge Rong, Yifan Nie, Vikang Shen and Zhang Xiong)</td>
</tr>
<tr>
<td>16:20pm - 16:45pm</td>
<td>Mathematical modelling for variations of inbreeding populations fitness with single and polygenic traits (Shuhao Sun, Fima Klebaner and Tianhai Tian)</td>
</tr>
<tr>
<td>16:45pm - 18:00pm</td>
<td>Poster Session / Exhibition</td>
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**Wednesday, January 18th, 2017**
<table>
<thead>
<tr>
<th>Time</th>
<th>Session 13: Analysis Tools</th>
<th>Session 14: Molecular Diagnosis with Omics Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>08:30am - 08:55am</td>
<td>A statistical method for the conservative adjustment of false discovery rate (q-value) (Yinglei Lai)</td>
<td>Discovering DNA methylation patterns for long non-coding RNAs associated with cancer subtypes (Xiaoke Ma, Liang Yu, Peizhuo Wang and Xiaofei Yang)</td>
</tr>
<tr>
<td>08:55am - 09:20am</td>
<td>Feature Selection Based on AUC and Variable Complementarity (Lei Sun, Jun Wang and Jinmao Wei)</td>
<td>Staged heterogeneity learning to identify conformational B-cell epitopes from antigen sequences (Jing Ren, Jianneng Song, John Ellis and Jinyan Li)</td>
</tr>
<tr>
<td>09:20am - 09:45am</td>
<td>Pysim-sv: a package for simulating structural variation data with GC-biases (Yuchao Xia, Yun Liu, Minghua Deng and Ruibin Xi)</td>
<td>GQSAR Modeling and Combinatorial library generation of 4-phenylquinazoline-2-carboxamide derivatives as Antiproliferative Agents in Human Glioblastoma Tumors (Debolina Goswami, Sukriti Goyal, Salma Jamal, Ritu Jain, Divya Wahi and Abhinav Grover)</td>
</tr>
<tr>
<td>09:45am - 10:10am</td>
<td>A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments (Vikas Bansal)</td>
<td>Gene Expression Profiling of Tumor Associated Macrophage after Exposure to Single Dose Irradiation (Wei-Hsiang Kung, Ching-Fang Yu, Andy Chi-Lung Lee, Chi-Dung Yang, Yu-Chen Liu, Fang-Hsin Chen and Hsien-Da Huang)</td>
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<tr>
<td>10:10am - 10:35am</td>
<td>Coffee Break (Lobby)</td>
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**Parallel Session 15: Networks and Interactions**

**Session Chair: Dr. Ruibin Xi**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session 15: Networks and Interactions</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:35am - 11:00am</td>
<td>Prior knowledge guided active modules identification: an integrated multi-objective approach (Weiqi Chen, Jing Liu and Shan He)</td>
</tr>
<tr>
<td>11:00am - 11:25am</td>
<td>An empirical fuzzy multifactor dimensionality reduction method for detecting gene-gene interactions (Sangseob Leem and Taesung Park)</td>
</tr>
<tr>
<td>11:25am - 11:50am</td>
<td>Node-based differential network analysis in genomics (Xiao-Fei Zhang, Le Ou-Yang and Hong Yan)</td>
</tr>
<tr>
<td>11:50am - 12:15pm</td>
<td>Selecting High-Quality Negative Samples for Effectively Predicting Protein-RNA Interactions (Zhanzhan Cheng, Kai Huang, Shuigeng Zhou, Hui Liu, Yang Wang and Jihong Guan)</td>
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</tbody>
</table>

**Session 16: Network Analysis**

**Session Chair: Prof. Jinyan Li**

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<thead>
<tr>
<th>Time</th>
<th>Session 16: Network Analysis</th>
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<tbody>
<tr>
<td>10:35am - 11:00am</td>
<td>Comparative network stratification analysis for identifying functional interpretable network biomarkers (Zhang Chuanchao, Liu Juan, Shi Qianqian, Zeng Tao and Chen Luoran)</td>
</tr>
<tr>
<td>11:00am - 11:25am</td>
<td>Construction of Condition-specific Pathway Interaction Network by Computing Shortest Paths on Weighted PPI (Li Hwan Moon, Sangsoo Lim, Kyuri Jo, Sangsoo Lee, Seokjun Seo and Sun Kim)</td>
</tr>
<tr>
<td>11:25am - 12:15pm</td>
<td>Active module identification in intracellular networks using a memetic algorithm with a new binary decoding scheme (Dong Li, Zhisong Pan, Guyu Hu, Zexuan Zhu and Shan He)</td>
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</tbody>
</table>

**Complimentary Lunch (Lobby)**

**Closing Remarks, Award Ceremony and Raffle Drawing (See You Next Year!)**